



SEQUENCE LISTING

<110> Haruo HANAWA

<120> VECTOR FOR GENE THERAPY AND METHOD OF QUANTIFYING TARGET PROTEIN IN MAMMAL OR CULTURED CELLS WITH THE ADMINISTRATION OF THE VECTOR FOR GENE THERAPY

<130> 0760-0347PUS1

<140> US 10/541,626

<141> 2005-07-07

<150> PCT/JP2003/016956

<151> 2003-12-26

<150> JP 2003-3967

<151> 2003-01-10

<160> 24

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<211> 11

<212> PRT

<213> Artificial Sequence

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<223> oligopeptide C19-29 region of glucagon of human, mouse or rat

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<212> DNA

<213> Artificial Sequence

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<223> DNA insert encoding rat IFN-r receptor, rat IgG Fc region and glucagon C19-29 region

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<221> CDS

<222> (13)..(1461)

<223> DNA insert encoding rat IFN-r receptor, rat IgG Fc region and glucagon C19-29 region

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99

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Pro Ala Pro Thr Asn Val Leu Ile Thr Ser Tyr Asp Leu Asn Pro Val			
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gta cat tgg aag cac cag aac gtg tcg cag gct gcc gtc ttc act gta			195
Val His Trp Lys His Gln Asn Val Ser Gln Ala Ala Val Phe Thr Val			
50	55	60	
cag gta aag atg tat cca gaa tac tgg act gat gcc tgc acc aac att			243
Gln Val Lys Met Tyr Pro Glu Tyr Trp Thr Asp Ala Cys Thr Asn Ile			
65	70	75	
gcc cat cat tat tgt aat atc tac aaa cac att tcc tat cct gac tca			291
Ala His His Tyr Cys Asn Ile Tyr Lys His Ile Ser Tyr Pro Asp Ser			
80	85	90	
tct gcc tgg gcc aga gtt aag gcc aag gtt gga caa aga gaa tct gcc			339
Ser Ala Trp Ala Arg Val Lys Ala Lys Val Gly Gln Arg Glu Ser Ala			
95	100	105	
tat gcg cag tca gaa gag ttt att atg tgc cga aag ggg aag gtt gga			387
Tyr Ala Gln Ser Glu Glu Phe Ile Met Cys Arg Lys Gly Lys Val Gly			
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ccg cct ggc ctg gac atc gga agg aag gaa gat cag ctg att gtc cac			435
Pro Pro Gly Leu Asp Ile Gly Arg Lys Glu Asp Gln Leu Ile Val His			
130	135	140	
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Ile Phe His Pro Lys Val Asn Val Ser Gln Glu Thr Met Phe Gly Asp			
145	150	155	
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Gly Asn Thr Cys Tyr Thr Phe Asp Tyr Thr Val Phe Val Lys His Tyr			
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Arg Ser Gly Glu Ile Leu His Thr Glu His Ser Val Leu Lys Glu Asp			
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Cys Ser Glu Thr Leu Cys Glu Leu Asn Ile Ser Val Ser Thr Leu Asn			
190	195	200	205
tcc aat tac tgt gtt tca gta gtt gga aag tcg tct ttc tgg caa gtt			675
Ser Asn Tyr Cys Val Ser Val Val Gly Lys Ser Ser Phe Trp Gln Val			
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Asn Thr Glu Thr Ser Lys Asp Ala Cys Ile Pro Phe Leu His Asp Asp			
225	230	235	
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Arg Glu Glu Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys Lys			

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cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc acg Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr	270	275	867
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tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat ttc agc Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His Phe Ser	290	295	915
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	315		
gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc ccc atc Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile	320	325	1011
	330		
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gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa ggc ttc Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys Gly Phe	385	390	1203
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aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac cac cat Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His	450	455	1395
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 65 70 75

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 Asn Asp Gln Val Thr Glu Val Cys Ala Thr Thr Phe Thr Val Lys Asn
 80 85 90

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 Thr Leu Gly Phe Leu Asp Asp Pro Phe Cys Ser Gly Thr Phe Asn Glu
 95 100 105

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cct gtg gcc ctc agg gag ctt atc gag gag ctg agc aac atc aca caa		147
Pro Val Ala Leu Arg Glu Leu Ile Glu Glu Leu Ser Asn Ile Thr Gln		
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Asp Gln Lys Thr Ser Leu Cys Asn Ser Ser Met Val Trp Ser Val Asp		
50 55 60		
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Leu Thr Ala Gly Gly Phe Cys Ala Ala Leu Glu Ser Leu Thr Asn Ile		
65 70 75		
tcc agt tgc aat gcc atc cac agg acc cag agg ata ttg aat ggc ctc		291
Ser Ser Cys Asn Ala Ile His Arg Thr Gln Arg Ile Leu Asn Gly Leu		
80 85 90		
tgt aac caa aag gcc tcg gat gtg gct tcc agc ccc cca gat acc aaa		339
Cys Asn Gln Lys Ala Ser Asp Val Ala Ser Ser Pro Pro Asp Thr Lys		
95 100 105		
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Ile Glu Val Ala Gln Phe Ile Ser Lys Leu Leu Asn Tyr Ser Lys Gln 110	115	120	125
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aaa ccc gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct Lys Pro Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro 255	260	265	270
819			
acc aag gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta Thr Lys Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val 270	275	280	285
867			
aaa ggc ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg Lys Gly Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly 290	295	300	305
915			
cag cca cag gaa aac tac aag aac act cca cct.acg atg gac aca gat Gln Pro Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp 305	310	315	320
963			
ggg agt tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp 320	325	330	325
1011			
cag cag gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac Gln Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His 330	335	340	345
1059			

335	340	345	
aac cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln 350	355	360	1107
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 ccc aga aac tgt gga ggt gat tgc aag cct tgt ata tgt aca ggc tca Pro Arg Asn Cys Gly Gly Asp Cys Lys Pro Cys Ile Cys Thr Gly Ser 30 35 40 45			
 gaa gta tca tct gtc ttc atc ttc ccc cca aag ccc aaa gat gtg ctc Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu 50 55 60			
 acc atc act ctg act cct aag gtc acg tgt gtt gtg gta gac att agc Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser 65 70 75			
 cag gac gat ccc gag gtc cat ttc agc tgg ttt gta gat gac gtg gaa Gln Asp Asp Pro Glu Val His Phe Ser Trp Phe Val Asp Asp Val Glu 80 85 90			
 gtc cac aca gct cag act cga cca cca gag gag gag ttc aac agc act Val His Thr Ala Gln Thr Arg Pro Pro Glu Glu Gln Phe Asn Ser Thr 95 100 105			
 ttc cgc tca gtc agt gaa ctc ccc atc ctg cac cag gac tgg ctc aat Phe Arg Ser Val Ser Glu Leu Pro Ile Leu His Gln Asp Trp Leu Asn 110 115 120 125			

ggc agg acg ttc aga tgc aag gtc acc agt gca gct ttc cca tcc ccc		435
Gly Arg Thr Phe Arg Cys Lys Val Thr Ser Ala Ala Phe Pro Ser Pro		
130	135	140
atc gag aaa acc atc tcc aaa ccc gaa ggc aga aca caa gtt ccg cat		483
Ile Glu Lys Thr Ile Ser Lys Pro Glu Gly Arg Thr Gln Val Pro His		
145	150	155
gta tac acc atg tca cct acc aag gaa gag atg acc cag aat gaa gtc		531
Val Tyr Thr Met Ser Pro Thr Lys Glu Glu Met Thr Gln Asn Glu Val		
160	165	170
agt atc acc tgc atg gta aaa ggc ttc tat ccc cca gac att tat gtg		579
Ser Ile Thr Cys Met Val Lys Gly Phe Tyr Pro Pro Asp Ile Tyr Val		
175	180	185
gag tgg cag atg aac ggg cag cca cag gaa aac tac aag aac act cca		627
Glu Trp Gln Met Asn Gly Gln Pro Gln Glu Asn Tyr Lys Asn Thr Pro		
190	195	200
205		
cct acg atg gac aca gat ggg agt tac ttc ctc tac agc aag ctc aat		675
Pro Thr Met Asp Thr Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Asn		
210	215	220
gtg aag aag gaa aaa tgg cag cag gga aac acg ttc acg tgt tct gtg		723
Val Lys Lys Glu Lys Trp Gln Gln Gly Asn Thr Phe Thr Cys Ser Val		
225	230	235
ctg cat gaa ggc ctg cac aac cac cat act gag aag agt ctc tcc cac		771
Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His		
240	245	250
tct ccg ggt aaa gcc caa gat ttt gtg cag tgg ttg atg aat acc		816
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Fc region and glucagons C19-29 region		
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Fc region and glucagons C19-29 region		
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Met Glu Ile Cys Trp Gly Pro Tyr Ser His Leu Ile Ser																
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ctc ctt ctc atc ctt ctg ttt cat tca gag gca gcc tgc cgc cct tct			99													
Leu	Leu	Leu	Ile	Leu	Leu	Phe	His	Ser	Glu	Ala	Ala	Cys	Arg	Pro	Ser	
15																
ggg aaa aga ccc tgc aag atg caa gcc ttc aga atc tgg gat act aac			147													
Gly	Lys	Arg	Pro	Cys	Lys	Met	Gln	Ala	Phe	Arg	Ile	Trp	Asp	Thr	Asn	
30																
cag aag acc ttt tac ctg aga aac aac cag ctc att gct ggg tac tta			195													
Gln	Lys	Thr	Phe	Tyr	Leu	Arg	Asn	Asn	Gln	Leu	Ile	Ala	Gly	Tyr	Leu	
50																
caa gga cca aat atc aaa cta gaa gaa aag ata gac atg gtg cct att			243													
Gln	Gly	Pro	Asn	Ile	Lys	Leu	Glu	Glu	Lys	Ile	Asp	Met	Val	Pro	Ile	
65																
gac ctt cat agt gtg ttc ttg ggc atc cac ggg ggc aag ctg tgc ctg			291													
Asp	Leu	His	Ser	Val	Phe	Leu	Gly	Ile	His	Gly	Gly	Lys	Leu	Cys	Leu	
80																
tct tgt gcc aag tct gga gat gat atc aag ctc cag ctg gag gaa gtt			339													
Ser	Cys	Ala	Lys	Ser	Gly	Asp	Asp	Ile	Lys	Leu	Gln	Leu	Glu	Glu	Val	
95																
aac atc act gat ctg agc aag aac aaa gaa gaa gac aag cgc ttt acc			387													
Asn	Ile	Thr	Asp	Leu	Ser	Lys	Asn	Lys	Glu	Glu	Asp	Lys	Arg	Phe	Thr	
110																
ttc atc cgc tct gag aaa ggc ccc acc acc agc ttt gag tca gct gcc			435													
Phe	Ile	Arg	Ser	Glu	Lys	Gly	Pro	Thr	Thr	Ser	Phe	Glu	Ser	Ala	Ala	
130																
tgt cca gga tgg ttc ctc tgc aca aca cta gag gct gac cgt cct gtg			483													
Cys	Pro	Gly	Trp	Phe	Leu	Cys	Thr	Thr	Leu	Glu	Ala	Asp	Arg	Pro	Val	
145																
agc ctc acc aac aca ccg gaa gag ccc ctt ata gtc acg aag ttc tac			531													
Ser	Leu	Thr	Asn	Thr	Pro	Glu	Glu	Pro	Leu	Ile	Val	Thr	Lys	Phe	Tyr	
160																
ttc cag gaa gac caa gcg gcc gtg ccc aga aac tgt gga ggt gat			579													
Phe	Gln	Glu	Asp	Gln	Ala	Ala	Val	Pro	Arg	Asn	Cys	Gly	Gly	Asp		
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tgc aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc			627													
Cys	Lys	Pro	Cys	Ile	Cys	Thr	Gly	Ser	Glu	Val	Ser	Ser	Val	Phe	Ile	
190																
ttc ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag			675													
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Thr	Ile	Thr	Leu	Thr	Pro	Lys	
210																
gtc acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat			723													
Val	Thr	Cys	Val	Val	Val	Asp	Ile	Ser	Gln	Asp	Asp	Pro	Glu	Val	His	
215																

225	230	235	
ttc agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg			771
240	245	250	
cca cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc Pro Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu			819
255	260	265	
ccc atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag Pro Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys			867
270	275	280	285
gtc acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa Val Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys			915
290	295	300	
ccc gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc Pro Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr			963
305	310	315	
aag gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa Lys Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys			1011
320	325	330	
ggc ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag Gly Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln			1059
335	340	345	
cca cag gaa aac tac aag aac act cca cct acg atg gac aca gat ggg Pro Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly			1107
350	355	360	365
agt tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Glu Lys Trp Gln			1155
370	375	380	
cag gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn			1203
385	390	395	
cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp			1251
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1 5 10

51

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Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala
15 20 25

99

aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa cct ttc cac
Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His
30 35 40 45

147

ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac tgc
Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys
50 55 60

195

gcc aac aca gaa att att gta aag ctt tct gat gga aga gag ctc tgt
Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys
65 70 75

243

ctg gac ccc aag gaa aac tgg gtg cag agg gtt gtg gag aag ttt ttg
Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu
80 85 90

291

aag agg gct gag aat tca gcg gcc ccg ggt aaa gcc caa gat ttt
Lys Arg Ala Glu Asn Ser Ala Ala Ala Pro Gly Lys Ala Gln Asp Phe
95 100 105

339

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Val Gln Trp Leu Met Asn Thr
110 115

369

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45

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